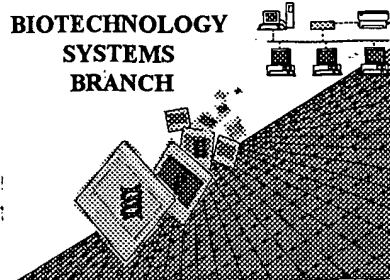


0570
12/7

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/821,782
Source: 01PE
Date Processed by STIC: 12/17/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,
Lobby, Room 1B03, Arlington, Virginia 22202

4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,
Arlington, VA 22202

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/821,782

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequences. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) . . .
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001
TIME: 15:11:29

pg 1-7

Input Set : A:\821782seq.oct.txt
Output Set: N:\CRF3\12172001\I821782.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Kumar Verma, Sunil
5 Singh, Lalji
7 <120> TITLE OF INVENTION: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION
9 <130> FILE REFERENCE: U-013365-9
11 <140> CURRENT APPLICATION NUMBER: 09/821782
13 <141> CURRENT FILING DATE: 2001-03-29
15 <160> NUMBER OF SEQ ID NOS: 255

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
19 <211> LENGTH: (25) 26 *shown*
21 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
27 <223> OTHER INFORMATION: Universal primer "mcb 398" for amplifying fragment of
cytochrome b gene
28 of animal species
30 <400> SEQUENCE: 1
E--> 32 taccatgagg acaaatatcta ttctg (25) 26
411 <210> SEQ ID NO: 19
413 <211> LENGTH: (328) 327
415 <212> TYPE: DNA
417 <213> ORGANISM: gz21CL
419 <220> FEATURE:
421 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard
(Neofelis
422 nebulosa) animal number 1 using primers mcb398 and mcb869
424 <400> SEQUENCE: 19
426 tgaatctgag gaggttctc agtagacaaa gccaccctga cagcattttt cgccttccac
427 ttcatcctcc catttatcat ctacgcctta gcagcagttc accttctatt tctccatgaa
E--> 428 aaggatcca ataaccctc aggaatggtta tccgattcag acaaaatccc gttccaccgc
E--> 429 tactatacaa tcaaagatat cctaggcctc ctagtcttaa ttctagcgt cactactatt
E--> 430 gttctattct cccagacct actaggagac cctgacaatt aactccgc caaccctcta
E--> 431 aataccctc cccatatcaa gcctgaat
434 <210> SEQ ID NO: 20
436 <211> LENGTH: (328) 327
438 <212> TYPE: DNA
440 <213> ORGANISM: gz22CL
442 <220> FEATURE:
444 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard
(Neofelis
445 nebulosa) animal number 2 using primers mcb398 and mcb869
447 <400> SEQUENCE: 20
449 tgaatctgag gaggttctc agtagacaaa gccaccctga cagcattttt cgccttccac
450 ttcatcctcc catttatcat ctacgcctta gcagcagttc accttctatt tctccatgaa
E--> 451 aaggatcca ataaccctc aggaatggtta tccgattcag acaaaatccc gttccaccgc

(25) 26

60
120
(180) 179
240
300
328
nos. off
due to
above error

60
120
(180) 179

see pg 2-3

E--> 452 tactatacaa tcaaagatat cctaggcctc ctagttctaa ttctagecgt cacactactt
E--> 453 gttctattct ccccagacct actaggagac cctgacaatt acactcccgc caaccctcta

240
300 nos.
off

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/821,782

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

E--> 454 aataccctc cccatatcaa gcctgaat

959 <210> SEQ ID NO: 45

961 <211> LENGTH: 472

963 <212> TYPE: DNA

965 <213> ORGANISM: Redunca fulvorufula

967 <400> SEQUENCE: 45

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970 tcccatacat cggcacaarc ctagttgaat gaatctgagg aggrttctca gtggataaag 120

971 caaccctcac tgcattcttc gccttcact ttatcctccc atttatcatc atagccctcg 180

972 ctatagtcca cctactattc ctccatgaaa caggatccaa caaccccaca ggggtttcat 240

E--> 973 cagayatgga caaatccca ttccaccnt actacacat caaagayatt ctagggtccc 300

974 tactactaat cctggcccta acactattag tactattcac ccctgaccta ctcgagacc 360

975 cggacaatta caccagca aaccactca acacacccc tcacatcaa ccagaatggt 420

E--> 976 atttcttatt ngcatagca atcctacgat caatcccaa taaactagga gg 472

1238 <210> SEQ ID NO: 59

1240 <211> LENGTH: 472

1242 <212> TYPE: DNA

1244 <213> ORGANISM: Balaenoptera bonaerensis

1246 <400> SEQUENCE: 59

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1249 tcccatacat tggtagacc ttagttgaat gaatctgagg tggcttctct gtagacaaag 120

1250 caacattaac acgctttttc gccttcact tcactcctccc ttctattatc ctatgattag 180

1251 caattgtcca cctcattttc ctccgcgaaa caggatccaa taaccccaca ggtattccat 240

1252 ctgatataga caaatccca ttccaccctt attacacaat caaagacatt ctaggcgccc 300

1253 tactactaat tctaacccta ctaaacactaa ccctattcgc acccgacctg ctcgagacc 360

E--> 1254 cggacaacta caccagca aaccactca gtacccagc acacattaaa ccagaatgat 420

1255 attttctatt cgcatacgca atcctacgat caatcccaa taaactaggc gg 472

1257 <211> LENGTH: 472

1259 <212> TYPE: DNA

1261 <213> ORGANISM: Balaenoptera borealis

W--> 1263 <210> SEQ ID NO:

E--> 1263 <400> SEQUENCE: 60

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1266 tcccatacat tggtagacc ctagtcgaat ggatctgagg cggtttctct gtagataaag 120

1267 caacactaac acgctttttt gccttcact tcattctccc ctctattatt ctatgactag 180

1268 caatggtcca cctcattttc ctccatgaaa caggatccaa caaccccaca ggtattccat 240

1269 cggacataga caaatccca ttccaccctt actacacagt taaagacatt ctaggcgccc 300

1270 tactactaat cctaacccta ctaataactaa ccctattcgc acccgacctg ctggagacc 360

1271 cagacaacta caccagca aatccactca gtacccagc acacattaaa ccagaatgat 420

E--> 1272 atttcttatt tgcatacgca atcctacgat caatcccaa caaattaggc gg 472

E--> 1275 <210> SEQ ID NO: 61

1277 <211> LENGTH: 472

1279 <212> TYPE: DNA

1281 <213> ORGANISM: Balaenoptera edeni

E--> 1283 <400> SEQUENCE: (60) 61 ← please edit

1285 taccctgagg acaaatatca ttttgaggcg caaccgtcat caccaacctc ttatcagcaa 60

1286 tcccatacat tggtagacc ctagtcgaat gaatctggg cggtttctct gtagataaag 120

1287 caacactaac acgctttttt gccttcact ttatcctccc ctctattatt ctatgactag 180

1288 caatggtcca cctcattttc ctccacgaaa caggatccaa taaccccaca ggtattccat 240

328

numbering
offsee
item 9
on
Even
summary
sheetdelete
hard page
break(hard page
breaks are
not
permitted
in
computer
readable
form)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

1289 ccaacataga caaaatccca ttccaccctt attacacaac taaagacatt ctaggcgccc 300
 1290 tactactaat cctaacccta ctaatgctaa cctatttcgt acccgacctt cttggagacc 360
 1291 cagacaacta cactccagca aatccactca gtaccccaac acacattaaa ccagaatgat 420
 1292 atttcctatt tgcatacgca atcctacgat caattcccaa caaattaggc gg 472
 2304 <210> SEQ ID NO: 13 *113 ← change*
 2306 <211> LENGTH: 472
 2308 <212> TYPE: DNA
 2310 <213> ORGANISM: Hyperoodon ampullatus
E--> 2312 <400> SEQUENCE: 113
 2314 taccctgagg acaaatatca ttctgaggcg caaccgtcat caccaatctc ctatccgcca 60
 2315 ttccctatat cggcactacc ctagttaga gaactctgagg tggtttctcc gtagacaaag 120
 2316 ccacattaac cgcgtttttc gccctccact ttatcctccc attcattatt ctagccctag 180
 2317 caatcgctcca cctactattc ctccatgaaa caggatccaa caatcccaca ggaattccat 240
 2318 ctgacataga caaaatcccg ttccacccat actacacaat caagacact ctaggggccc 300
 2319 tattactaat cctagtccca ctacacattaa cctatttcgc acccgacctt ctaggagacc 360
 2320 ctgataacta taccacagca aacccactca gcaactccagc acacatcaaa ccagaatggt 420
 2321 acttcttatt tgcatacgca atcctacggt caatccctaa caaactagga gg 472
E--> 2324 <210> SEQ ID NO: 114
 3404 <210> SEQ ID NO: 169
 3406 <211> LENGTH: 472
 3408 <212> TYPE: DNA
 3410 <213> ORGANISM: Afropavo congensis
 3412 <400> SEQUENCE: 169
 3414 tcccatgagg ccaaatatca ttctgagggg caactgtcat caaaaacctt tactcagcaa 60
 3415 tccctatat tggtaaaacc ctagttaga ggcctgagg aggattctca gttgacaacc 120
 3416 caaccctcac cgcattcttc gccctacact ttcttctccc ctttctaatt gcgggaatta 180
 3417 caattatcca cctcacattc ctccatgaat caggctcaaa caaccactg ggcattctcat 240
 3418 ccaattcaga taaaatccca ttccaccgt actactccct caagatatc ctaggcttag 300
 3419 cactcatgct cattccattc ctgacactag ccctactctc cccaacctc ttaggtgatc 360
 3420 cagaaaactt caccacagca aaccctctag taactcccc acacattaaa ccagaatggt 420
 E--> 3421
 atttcttatt tgcctatgcc atccttcgct caatcccaaa caaactagga gg 472
 3423 <211> LENGTH: 472
 3425 <212> TYPE: DNA
 3427 <213> ORGANISM: Pavo muticus
E--> 3429 <210> SEQ ID NO:
E--> 3429 <400> SEQUENCE: 170
 3431 tcccatgagg tcaaatgtca ttctgagggg caactgttat caaaaatcta ttctcagcaa 60
 3432 tccctatat tggacaaacc ctagttaga gagcctgagg ggcattctca gtcgacaacc 120
 3433 caaccctcac cgcattcttc gccctacact ttctcctccc ctttgtaatc gcaggaatta 180
 3434 caattatcca cctcacattc ctccatgaat caggctcaaa taatccacta ggcattctcat 240
 3435 ccaactcaga caaaattccg ttccacccat actactccct caagatatc ctaggcttaa 300
 3436 ctcttatatt tatccattc ctaacactag ccctattctc cccaatctc ctaggtgacc 360
 3437 cagaaaactt taccacagca aaccctctag taaccccc gcacattaaa ccagaatgat 420
E--> 3438 atttcttatt tgcctacgcc atccttcggt caatcccaaa caaactagga gg 472
E--> 3441 <210> SEQ ID NO: 171
 4283 <210> SEQ ID NO: 214
 4285 <211> LENGTH: 23 *22 (p.5)*
 4287 <212> TYPE: DNA
 4289 <213> ORGANISM: Artificial Sequence

472<210> 170

delete hard
 page break code

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/821,782

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

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4291 <220> FEATURE:
4293 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b
4294     gene of animal species in polymerase chain reaction
4296 <400> SEQUENCE: 214
E--> 4298 tagtagaat gaatctgagg agg                                22
4301 <210> SEQ ID NO: 215
4303 <211> LENGTH: 23 22
4305 <212> TYPE: DNA
4307 <213> ORGANISM: Artificial Sequence
4309 <220> FEATURE:
4311 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b
4312     gene of animal species in polymerase chain reaction
4314 <400> SEQUENCE: 215
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4319 <210> SEQ ID NO: 216
4321 <211> LENGTH: 472
4323 <212> TYPE: DNA
4325 <213> ORGANISM: Aepyceros melampus
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E--> 4330 tcccatacat tggtagaaac ctagtagaat gaatctgagg aggtttttca gtagacaaag        120
E--> 4331 caacccttac cgcatttttc gcyttccact tcatcyttcc attcatcatt gcggcactag        180
4332 ccatagtcca cctactcttt cttcacgaaa caggatctaa caaccctaca ggaatcttat        240
4333 cagattcaga taaaattcca ttccaccctt actatactat traagacatc ctagggaatcc        300
4334 tattaataat tctagtccta atactcctag tactattcat acccgaccta ctaggagacc        360
E--> 4335 cagacaanna catccccgca aaccactca acaccctcc ccacatcaag cccgaatggt        420
E--> 4336 acttctgtt ngcatagcga atcctacgat caatcccca taaactagga gg        472
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4344 <213> ORGANISM: Oreotragus oreotragus
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4350 caacccttac cgcattcttt gcctttcact tcatctttcc atttatcatc gcagccctag        180
4351 ccatagtaca cctactcttt ctccacgaaa cagggtccaa taaccccaca ggaatctcat        240
4352 cagacacaga caaaatccca ttctatcctt attacacaat caaagatatc ctaggcgccc        300
4353 tattactaat tctagcttta ttactcttag tattattcac acctgacctt cttggagacc        360
4354 cagataacta caccacagca aaccactca acactcccc tcacattaaa ccagaatggt        420
E--> 4355 atttncatt ngcatatgca atcctacgat caatcccca taaactagga gg        472
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4520 <211> LENGTH: 472
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4524 <213> ORGANISM: Bison bonasus
4526 <400> SEQUENCE: 226
4528 taccatgagg acaaatatca ttttgaggag caacagtcac taccaacctc ctatcagcaa        60
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4530 caacccttac cgcatttttc gctttccact ttatctctcc atttattatc atagcaattg        180
4531 ccatagttca cctactattc ctccacgaaa caggttctaa caatccaaca ggaatttcct        240

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see Item 9 on Eva
summary
sheet

Item 9

P. 6

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/821,782

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

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4533 tattactaat tctaactcta atactactag tactattcgc accggacctc ctcgagagacc      360
4534 cagataacta caccacagca aatccactta acacacctcc ccacatcaaa cccgaatgat      420
E--> 4535 acttcttatt tgcatangca attttacggg caatccccaa caaactagga gg item 9      472
4794 <210> SEQ ID NO: 240
4796 <211> LENGTH: 472
4798 <212> TYPE: DNA
4800 <213> ORGANISM: Rupicapra rupicapra
4802 <400> SEQUENCE: 240
4804 taccatgagg acagatatca ttctggggag caacagttat taccaacctc ctctcagcga      60
4805 tcccgatatat tggcacagac ttagtcgaat gaatctgagg aggccttctcg gtagacaagg      120
4806 ctaccctcac ccgattcttt gccttccact tcactctccc atttatcatt gcagccttag      180
4807 ccctagtcca cctactcttc ctccacgaaa caggatctaa caaccccaaca ggaatcccat      240
E--> 4808 cagatgcgga caaaatccca tttnacccct attataccat caaagacatt ctgggcgcca      300
E--> 4809 tactactaat cctcaccctc atactactag tactattnac acctgacctc ctcgagagacc item 9      360
4810 cagataatta caccacagcg aaccactca acacaccccc tcacattaaa cccgagtgat      420
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4875 <211> LENGTH: 472
4877 <212> TYPE: DNA
4879 <213> ORGANISM: Ovis vignei
4881 <400> SEQUENCE: 244
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4885 ctaccctcac ccgatttttc gcctttcact ttattttccc attcatcatc gcagccctcg      180
4886 ctatagttca cctactcttc ctccacgaaa caggatccaa taaccccaaca ggaattccat      240
E--> 4887 cggacacaga caaaatcccc ttcnnnnnnn nnnnnnnnat taaagacatt ctgggtgcca item 9      300
4888 tcctactaat cctcatcctc atgctgctag tactattcac gcctgactta cttggagacc      360
4889 cagacaacta caccacagca aaccacttta acactcccc tcacatcaaa cctgaatgat      420
4890 atttcctatt tgcatatgca atcttacgat caatccctaa taaactagga gg      472
5089 <210> SEQ ID NO: 255
5091 <211> LENGTH: 472
5093 <212> TYPE: DNA
5095 <213> ORGANISM: Cervus elaphus canadensis
E--> 5097 <400> 255
5099 taccatgagg acaaatatca ttctgaggag caacagtcac taccaacctt ctctcagcaa      60
5100 ttccatacat tggcacaaac ctagtgcgaat gggctctgagg aggccttttca gtagataaaag      120
5101 caaccctaac ccgattcttc gctttccact ttattctccc atttatcatc gcagcactcg      180
5102 ctatagtaca cttactcttc cttcacgaga caggatctaa taacccaaca ggaatcccat      240
5103 cagacgcaga caaaatcccc ttccaccctt actatacgat taaagatatc ttaggtatct      300
5104 tacttctaata actcttccta atattactag tattattcgc accagatctg cttggagacc      360
5105 cagacaacta taccacagca aatccactca acacaccccc tcacattaaa cctgaatgat      420
5106 atttcctatt tgcatagcga atcctacgat caattcccaa caaactagga gg      472

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see next page

09/21, 782

7

<210> 255

<211> 472

<212> DNA

<213> Cervus elaphus canadensis

~~<220>~~

<400> AB021096 → <2237

move up to <2237 line

<400> always has the sequence ID number as a response

<400> 255

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001

TIME: 15:11:31

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

L:32 M:254 E: No. of Bases conflict, LENGTH:Input:25 Counted:26 SEQ:1
 L:32 M:252 E: No. of Seq. differs, <211>LENGTH:Input:25 Found:26 SEQ:1
 L:428 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:19
 M:254 Repeated in SeqNo=19
 L:431 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:327 SEQ:19
 L:451 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:20
 M:254 Repeated in SeqNo=20
 L:454 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:327 SEQ:20
 L:973 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:45
 M:340 Repeated in SeqNo=45
 L:1255 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:474 SEQ:59
 L:1255 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
 L:1255 M:252 E: No. of Seq. differs, <211>LENGTH:Input:472 Found:474 SEQ:59
 L:1263 M:282 W: Numeric Field Identifier Missing, <210> is required.
 L:1263 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:59 differs:60
 L:1275 M:214 E: (33) Seq.# missing, SEQ ID NO:60
 L:1283 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:61 differs:60
 L:2312 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:113
 L:2324 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 14 thru 113
 L:3421 M:254 E: No. of Bases conflict, LENGTH:Input:170 Counted:474 SEQ:169
 L:3421 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
 L:3421 M:252 E: No. of Seq. differs, <211>LENGTH:Input:472 Found:474 SEQ:169
 L:3429 M:282 W: Numeric Field Identifier Missing, <210> is required.
 L:3429 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:169 differs:170
 L:3441 M:214 E: (33) Seq.# missing, SEQ ID NO:170
 L:4298 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:22 SEQ:214
 L:4316 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:22 SEQ:215
 L:4330 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:216
 M:340 Repeated in SeqNo=216
 L:4355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:217
 L:4535 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:226
 L:4808 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:240
 M:340 Repeated in SeqNo=240
 L:4887 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:244
 L:5097 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:255 differs:254